

1381 agatttggag gatttggggg ctgtagccc cccagtcagt ggagacttaa ccaaagagga 1441 catagatetg attgacatec tttggcgaca ggatattgat etgggggetg ggcgtgaggt 1501 ttttgactat agtcaccgcc agaaggagca ggatgtggag aaggagctgc gagatggagg 1561 cgagcaggac acctgggcag gcgagggcgc ggaagctctg gcacggaacc tgctagtgga 1621 tggagagact ggggagagct tccctgcaca gtttccagca gacatttcca gcataacaga 1681 agcagtgcct agtgagagtg agcccctgc tcttcaaaac aacctcttgt ctcctcttct 1741 gaccgggaca gagtcaccat ttgatttgga acagcagtgg caagatctca tgtccatcat 1801 ggaaatgcag gccatggaag tgaacacatc agcaagtgaa atcctgtaca gtgcccctcc 1861 tggagaccca ctgagcacca actacagcct tgcccccaac actcccatca atcagaatgt 1921 cagectgeat caggegteec tgggggggetg cagecaggae ttettaetet teageceega 1981 ggtggaaage etgeetgtgg eeagtagete eacgetgete eegttggeee eeageaatte 2041 taccagecte aactecacet teggeteeae caacetgaca gggetettet ttecacecea 2101 gctcaatggc acagccaatg acacagcagg cccagagctg cctgaccctt tgggggggtct 2161 gttagatgaa gctatgttgg atgagatcag ccttatggac ctggccattg aagaaggctt 2221 taaccetgtg caggeetece agetggagga ggaatttgae tetgaeteag geettteett 2281 agactegage catagecett etteectaag cagetetgaa ggeagttett eetettette 2341 etectectet teetettett eetetgette tteetetgee tetteeteet titetgagga 2401 aggtgcggtt ggctacagct ctgactctga gaccctggat ctggaagagg ccgagggtgc 2461 tgtgggctac cagcctgagt attccaagtt ctgccgcatg agctaccagg atccagctca 2521 gctctcatgc ctgccctacc tggagcacgt gggccacaac cacacataca acatggcacc 2581 cagtgccctg gactcagccg acctgccacc acccagtgcc ctcaagaaag gcagcaagga 2641 gaagcagget gaetteetgg acaagcagat gagcegggat gagcaccgag cccgagccat 2701 gaagateet tteaceaatg acaaaateat caacetgeet gtggaggagt teaatgaact 2761 gctgtccaaa taccagttga gtgaagccca gctgagcctc atccgagaca tccggcgccg 2821 gggcaagaac aagatggcgg cgcagaactg ccgcaagcgc aagctggaca ccatcctgaa 2881 tetggagegt gatgtggagg acetgeageg tgacaaagee eggetgetge gggagaaagt 2941 ggagtteetg egeteeetge gacagatgaa geagaaggte cagageetgt accaggaggt 3001 gtttgggcgg ctgcgagatg agaacggacg accetactcg cccagtcagt atgcgctcca 3061 gtacgccggg gacggcagtg tcctcctcat cccccgcacg atggccgacc agcaggcccg 3121 gcggcaggag aggaagccaa aggaccggag aaagtgagcc tggggaagaa gggggtttga 3181 ageccaccaa gaccgaaact ggagaaggge tggacctgga cetggacetg gacctacage 3241 ggggacttaa atgccttctt atccaatata tcttctcaga tgggatgact gcgggtcagt 3301 gtacaggaag aggcaggcac tggctggctc agctccactc gggtggagtg gaagtggcca 3361 gaccatttag acggacaggg tecteacect acceetttee tgtgaggeag gggtggtggt 3421 ggagttgctg gaggtagagg agctatgtgg agcaaaggcc gacagagggg aaggaatgga 3481 cctgtgagag gaagggaagg tggcagaaag tctcatttca ggaaggaggg atagaaggaa 3541 ggaaggaagg aaccccccc ccccgaaaa aaaaatcaaa gcgggaagaa aatcagaggg 3601 aaggttaagg ttggctctgg ccaggattcc aggcagcagg ttggagtgac tggtgggcct 3661 agatcactgg tgtgataaac cccatttcac cccggggggg gtggggtaca cagacacagg 3721 gtgggggtgg ggaggggcgg tgttaactct ttctgctcct tgcattttga catccctgaa 3781 ggggagetet tggatateat tggccatgtt teaategaat ggagecactg ggccccaaca 3841 ctggctttga gatttagagt caaagggtag agtgaacagg aaagggtcac gtggtcccat 3901 gttgcaacag ccccaacata cgcatgtcat tcactgcctt gccactccat ctccctccgt 3961 getecageca eccetgaget gaggetecea ttgtetecat cagagectge atgtgtatge 4021 cgtcctcccc tggtccggtg tttgtgttcc ccacccctca cagactgcct gagctcttct 4081 gtaagetggg gtagggtgat ggeagtgete egggaaetgg geetgeagee tteetettet 4141 gggactgctg tgaggcagag gaatgatgga gaatctagtg tagcagcctc caggcaggat 4201 teageacaac aetggggagt caccettece tegggeetet geetaceaac aactgggett 4261 atcactggga aaacacaaaa aattacacaa cccagcaaca acaaaagaac tagtcctctt 4321 agaatttett gegetttgat tittttaggg ettgtgeeet gitteaetta tagggtetag 4381 aatgettgtg ttgagtaaaa aggagatgee caatatteaa agetgetaaa tgttetettt 4441 gccataaaga ctccgtgtaa ctgtgtgaac acttgggatt tttctcctct gtcccgaggt 4501 cgtcgtctgc tttctttttt gggtttcttt ctagaagatt gagaagtgca tatgacaggc 4561 tgagageacc tececaaaca cacaagetet cagecacagg cagettetee acagececag 4621 cttcqcacag gctcctggag ggctgcctgg gggaggcaga catgggagtg ccaaggtggc 4681 cagatggttc caggactaca atgtctttat ttttaactgt ttgccactgc tgccctcacc 4741 cctgcccggc tctggagtac cgtctgcccc agacaagtgg gagtgaaatg ggggtggggg 4801 gaagcactga ttcccaqtta gggggtgcct aactgagcag tagggataga aggtgtgaac 4861 ctgggagtgc ttttataaat tattttcctt gtagatttta tttttaattt atctctgtga NCBI Sequence Viewer

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4981 aatggatgat to

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Oct 29 2003 07:23:28

Sequences producing significant alignments:	(bits)		
qi 542952 pir A49672 transcription factor Nrf1 - human >gi	<u>1210</u>	0.0	
qi 21748606 dbi BAC03440.1 FLJ00380 protein [Homo sapiens]	<u>1200</u>	0.0	
gi 4505379 ref NP 003195.1 nuclear factor (erythroid-deriv	<u>1195</u>	0.0	<u> </u>
gi[31982173 ref[NP 032712.2] nuclear factor, erythroid deri	<u>1166</u>	0.0	<u> </u>
gil6831586 spl061985 NFL1 MOUSE Nuclear factor erythroid 2		0.0	1

·		
gil34873489 ref XP 340887.1 similar to nuclear factor, ery	1143	0.0
3-1	1038	0.0
	649	0.0
gi 520471 gb AAA20466.1 transcription factor LCR-F1		-
gi 37590281 gb AAH59314.1 Unknown (protein for MGC:68992)	<u>640</u>	
gi 12836061 dbi BAB23483.1 unnamed protein product [Mus mu	<u>498</u>	e-139
gi 5441517 emb CAB46813.1 bZIP protein [Canis familiaris]	<u>310</u>	5e-83
gi 37682103 gb AA097978.1 nuclear factor-like 1 [Danio rerio]	<u>299</u>	2e-79
gi 3108203 gb AAC40108.1 nuclear factor erythroid-related	<u> 295</u>	1e-78
gi 21918831 ref NP 004280.3 nuclear factor (erythroid-deri	<u>237</u>	7e-61
gi 20912933 ref XP 126805.1 similar to Nuclear factor eryt	231	3e-59 🗌
gi Louizou i i i i i i i i i i i i i i i i i i i	231	4e-59
	228	4e-58
gi 4521225 dbi BAA76288.1 NF-E2-related factor 3 [Homo sap		1e-57
gil29351561 gb AAH49219.1 NFE2L3 protein [Homo sapiens]	<u>226</u>	
gil6563268 gb AAF17228.1 NFE2-related factor 1 [Homo sapiens]	<u>223</u>	1e-56
gi 37545874 ref XP 017121.4 similar to nuclear factor (ery	<u>214</u>	6e-54
gi 6754834 ref NP 035033.1 nuclear factor, erythroid deriv	<u>198</u>	3e-49 🔛
gi 34855866 ref XP 231763.2 similar to Nrf3 [Rattus norveg	<u> 186</u>	2e-45
gi 28277788 gb AAH45852.1 Similar to nuclear factor (eryth	<u> 182</u>	2e-44
gi 2137618 pir 149261 p45 NF-E2 related factor 2 - mouse >	182	2e-44
gi 33504557 ref NP 878309.1 nuclear factor (erythroid-deri	182	2e-44
	182	3e-44
<u>3: 1 1 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 </u>	180	9e-44
	177	7e-43
gi 2134328 pir 50224 erythroid cell transcription factor		1e-42
gi 27695228 gb AAH43997.1 Similar to nuclear factor (eryth	<u>176</u>	
gi 2136301 pir 159340 transcription factor Nrf2 - human >g	<u>175</u>	3e-42
gi 33469085 ref NP 032711.1 nuclear factor, erythroid deri	<u>174</u>	4e-42
gi 20903673 ref XP 128255.1 nuclear factor, erythroid deri	<u>174</u>	5e-42
gi 20149576 ref NP 006155.2 nuclear factor (erythroid-deri	<u>174</u>	5e-42
gi 5453774 ref NP 006154.1 nuclear factor (erythroid-deriv	<u> 174</u> -	6e-42 l
gil1082640 pir A54692 transcription factor NF-E2 45K chain	<u>172</u>	1e-41
gi 506818 gb AAA35612.1 leucine zipper protein	<u>172</u>	3e-41
gi 31200287 ref XP 309091.1 ENSANGP00000003712 [Anopheles	<u> 167</u>	7e-40
gi 28077099 ref NP 778208.1 nuclear factor (erythroid-deri	<u>162</u>	2e-38
gi 24649238 ref NP 732834.1 cap-n-collar CG17894-PB [Droso	<u>153</u>	1e-35 🗔
<u>gi 24649240 ref NP 732835.1 </u> cap-n-collar CG17894-PA [Droso	<u>151</u>	4e-35
	<u>151</u>	4e-35
	151	4e-35
	151 151	4e-35
gil7511827 pir T13936 collar protein isoform C - fruit fly	151 151	5e-35
gi 3859887 gb AAC72897.1 cap 'n' collar isoform B [Drosoph	150	1e-34
gi 103368 pir A33111 segmentation protein cnc - fruit fly		1e-34 1e-34
gil1352098 sp P20482 CNC DROME Segmentation protein cap'n'c	<u>149</u>	
gi 157074 gb AAB59246.1 segmentation protein [Drosophila m	<u>148</u>	3e-34
gi 34868687 ref XP 345884.1 similar to transcription facto	<u>129</u>	3e-28
gi 34867531 ref XP 221712.2 similar to Bach1 [Rattus norve	94	1e-17
gi[2565400]gb[AAB84100.1] transcription regulator protein [<u>93</u>	2e-17
gil4502353 ref INP 001177.1 BTB and CNC homology 1, basic 1	<u>93</u>	2e-17
gi 6680764 ref NP 031546.1 BTB and CNC homology 1 [Mus mus	<u>92</u>	2e-17
gi 7768712 dbi BAA95505.1 transcription regulator protein	<u>92</u>	3e-17
gill3540490[ref[NP 068585.1] BTB and CNC homology 1, basic	84	9e-15
gill3898847 gb AAK48898.1 BACH2 transcription factor [Homo	84	9e-15 🗔
gi 30109320 qb AAH51242.1 Similar to BTB and CNC homology	84	1e-14
<u></u>	84	1e−14 🗔
	-	5e-12
		2e-11
	64	1e-08
gi 5739132 gb AAD50356.1 Cap'n'collar protein [Thermobia d		1e-06
gi 25148068 ref NP 741404.1 the Binding Domain Of Skn-1 In	_57	
gi 25148072 ref NP 741406.1 the Binding Domain Of Skn-1 In	<u>57</u>	1e-06
gi 25148077 ref NP 741405.1 the Binding Domain Of Skn-1 In	<u>57</u>	2e-06 l

	EG	3e-06 🖾
gi[3318844]pdb[1SKN]P Chain P, The Binding Domain Of Skn-1	<u>56</u> 52	3e-05
gil17565016 ref NP 503719.1 predicted CDS, the Binding Dom		
gi 15636685 gb AAL02138.1 transcription factor AP-1 [Branc	44	0.011
gi12497469 sp P79703 JUNB CYPCA TRANSCRIPTION FACTOR JUN-B	44	0.014
gil29823878[emb]CAD56858.1] JunB protein [Takifugu rubripes]	<u>43</u>	0.023
gil2118496lpir11151606 gene c-jun protein - African clawed	42	0.030
gil29823880 emb CAD56859.1 FJun protein [Takifugu rubripes]	<u>42</u>	0.031
gil26353686 dbj BAC40473.1 unnamed protein product [Mus mu	<u>42</u>	0.032
gi152759 emb CAA31252.1 unnamed protein product [Mus muscu	_42	0.032
gi 6680512 ref NP 032442.1 Jun-B oncogene [Mus musculus] >	42	0.032
gi 31419519 gb AAH53234.1 Unknown (protein for MGC:64066)	42	0.032
gi 5650726 emb CAB51637.1 c-Jun protein [Xenopus laevis]	42	0.034
gi 31339308 dbj BAC77044.1 c-Jun protein [Carassius auratus]	42	0.034
gi 11177866 ref NP 068608.1 jun B proto-oncogene [Rattus n	42	0.035
diliti//866/retine 066000.il Juli b proto-cheogene that tas in the	42	0.035
gil710348 gb AAA74916.1 transcription factor junB	42	0.036
gi 4504809 ref NP 002220.1 jun B proto-oncogene [Homo sapi	42	0.036
gi 14495707 gb AAH09465.1 Jun B proto-oncogene [Homo sapiens]		0.036
gil29823874[emb CAD56856.1] c-Jun protein [Takifugu rubripes]	42	0.030
gi 3023298 sp P56432 AP1 PIG Transcription factor AP-1 (Act	42	
<u>gi 225973 prf 1404381A</u> c-jun oncogene	42	0.037
gi 4758616 ref NP 002219.11 v-jun avian sarcoma virus 17 on	42	0.037
<u>gi 226129 prf 1411298A</u> c-jun gene	42	0.037
gi 6754402 ref NP 034721.1 Jun oncogene; activator protein	_42	0.037
gi 11177864 ref NP 068607.1 v-jun sarcoma virus 17 oncogen	42	0.037
gil68985lpirllTVHUJN transcription factor AP-1 - human	<u>42</u>	0.037
gil135295 sp P18870 AP1 CHICK TRANSCRIPTION FACTOR AP-1 (PR	42	0.038
gi 21313434 ref NP 084356.1 RIKEN cDNA 1700012K17; androge	<u>42</u>	0.040 [
gil12838749 dbi BAB24315.1 unnamed protein product [Mus mu	42	0.040
91112330110100112212		

Alignments

transcription factor Nrf1 - human >qi|542952|pir||A49672 qi|14714932|qb|AAH10623.1| NFE2L1 protein [Homo sapiens] Length = 742Score = 1210 bits (3131), Expect = 0.0Identities = 652/740 (88%), Positives = 652/740 (88%) MLSLKKYLTEGLLOFTILLSLIGVRVDVDTYLTSOLPPLREIILGPSSAYTOTOFHNLRN 60 Query: 1 MLSLKKYLTEGLLOFTILLSLIGVRVDVDTYLTSOLPPLREIILGPSSAYTOTOFHNLRN MLSLKKYLTEGLLOFTILLSLIGVRVDVDTYLTSQLPPLREIILGPSSAYTQTQFHNLRN 60 Sbict: 1 TLDGYG1HPKS1DLDNYFTARRLLSOVRALDRFOVPTTEVNAWLVHRDPEGSVSGSQPNS 120 Query: 61 TLDGYGIHPKSIDLDNYFTARRLLSQVRALDRFQVPTTEVNAWLVHRDPEGSVSGSQPNS TLDGYGIHPKSIDLDNYFTARRLLSOVRALDRFOVPTTEVNAWLVHRDPEGSVSGSQPNS 120 Sbjct: 61 Ouery: 121 GLALESSSGLODVTGPDNGVRESETEOGFGEDLEDLGAVAPPVSGDLTKEDIDLIDILWR 180 GLALESSSGLODVTGPDNGVRESETEOGFGEDLEDLGAVAPPVSGDLTKEDIDLIDILWR

Sbjct: 121 GLALESSSGLODVTGPDNGVRESETEOGFGEDLEDLGAVAPPVSGDLTKEDIDLIDILWR 180

Ouery: 181 ODIDLGAGREVFDYSHROKEODVEKELRDGGEODTWAGEGAEALARNLLVDGETGESFPA 240

Sbjct: 181 ODIDLGAGREVFDYSHROKEODVEKELRDGGEODTWAGEGAEALARNLLVDGETGESFPA 240

ODIDLGAGREVFDYSHROKEODVEKELRDGGEODTWAGEGAEALARNLLVDGETGESFPA

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